

**BLAST2 Search Results****EXHIBIT B**Docket No.: PF-0609 USN
USSN: 09/806,267

Sequences

Help

Retrieval

BLAST2

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ClustalW

GCG Assembly

Phrap

Translation

BLAST2 Manual

Confidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: blastp**Sequence ID(s):**☐ 135698CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 135698CD1
(234 letters)

Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<input checked="" type="checkbox"/> <u>g27728685</u> anti-rabies SOJA immunoglobulin kappa light chain [444	e-124
<input checked="" type="checkbox"/> <u>g21619606</u> similar to anti TNF-alpha antibody light-chain Fab	436	e-121
<input checked="" type="checkbox"/> <u>g17645754</u> unnamed protein product [Homo sapiens]	434	e-121
<input checked="" type="checkbox"/> <u>g17644683</u> unnamed protein product [Homo sapiens]	434	e-121
<input checked="" type="checkbox"/> <u>g21410096</u> Unknown (protein for MGC:22645) [Homo sapiens]	431	e-119
<input checked="" type="checkbox"/> <u>g17645758</u> unnamed protein product [Homo sapiens]	430	e-119
<input checked="" type="checkbox"/> <u>g17644687</u> unnamed protein product [Homo sapiens]	430	e-119
<input checked="" type="checkbox"/> <u>g16741061</u> Similar to immunoglobulin kappa constant [Homo sapi	430	e-119
<input checked="" type="checkbox"/> <u>g23683336</u> immunoglobulin kappa light chain [Homo sapiens]	423	e-117
<input checked="" type="checkbox"/> <u>g21669465</u> immunoglobulin kappa light chain VLJ region [Homo s	415	e-115

>g27728685 anti-rabies SOJA immunoglobulin kappa light chain [Homo sapiens]
Length = 234

Score = 444 bits (1131), Expect = e-124
Identities = 217/234 (92%), Positives = 224/234 (94%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP 60
MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATL+CRASQ+ S YLAWYQQKP
Sbjct: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP 60

Query: 61 GQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFGQ 120
GQAPRLLIYD SNRATGIP RFSGSGSGTDFTL+IS LEPED A+YYCQQ F P+TFGQ
Sbjct: 61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120

Query: 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
GT++E KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
Sbjct: 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180

Query: 181 ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

>g21619606 similar to anti TNF-alpha antibody light-chain Fab
fragment [Homo sapiens]
Length = 236

Score = 436 bits (1110), Expect = e-121
Identities = 219/236 (92%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQK 59
ME PAQLLFLLLLWLPD+TGE VLTQSP TSLSPGERATLSCRASQS+SS YLAWYQQK
Sbjct: 1 METPAQLLFLLLLWLPDSTGENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTT-PYTF 118
PGQAPRLLIY S+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQY T+ P TF
Sbjct: 61 PGQAPRLLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPITF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGTRL+IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
Sbjct: 121 GQGTRLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17645754 unnamed protein product [Homo sapiens]
Length = 236

Score = 434 bits (1105), Expect = e-121
Identities = 217/236 (91%), Positives = 226/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
ME PAQLLFLLLLWLPD TTGEIVLTQSP TSLSPGERATLSCRASQ++ SSYLAWYQQK
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118
PGQAP LLIY AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F
Sbjct: 61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17644683 unnamed protein product [Homo sapiens]

Length = 236

Score = 434 bits (1105), Expect = e-121

Identities = 217/236 (91%), Positives = 226/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQK 59
ME PAQLLFLLLLWLPD TTGEIVLTQSP TLSLSPGERATLSCRASQ++ SSYLAWYQQK
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPGTLSPGERATLSCRASQNIRSSYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118
PGQAP LLIY AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F
Sbjct: 61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g21410096 Unknown (protein for MGC:22645) [Homo sapiens]
Length = 234

Score = 431 bits (1096), Expect = e-119

Identities = 210/234 (89%), Positives = 224/234 (94%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP 60
MEAPAQLLFLLLLWLPD TTGEIV+TQSPATLS+SPGERATLSCRASQSV+S LAWYQQ P
Sbjct: 1 MEAPAQLLFLLLLWLPD TTGEIVMTQSPATLSVSPGERATLSCRASQSVTSNLAWYQQTP 60

Query: 61 GQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFGQ 120
GQ+PRL+IY AS+RA+G+P RFSGSGSGT+FTLTIS L+ ED A+YYCQQY P+TFGQ
Sbjct: 61 GQSPRLVIYGASSRASGVPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYNKWPHTFGQ 120

Query: 121 GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
GT+L+IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
Sbjct: 121 GTKLDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180

Query: 181 ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 ESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

>g17645758 unnamed protein product [Homo sapiens]
Length = 236

Score = 430 bits (1095), Expect = e-119

Identities = 216/236 (91%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSY-LAWYQQK 59
ME PAQLLFLLLLWLPD TTGEIVLTQSP TLSLSPGERATLSCRASQS+SS LAWYQQK
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPGTLSPGERATLSCRASQSISSSSLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118
PGQAP LLI+ AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F
Sbjct: 61 PGQAPGLLIIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g17644687 unnamed protein product [Homo sapiens]
Length = 236

Score = 430 bits (1095), Expect = e-119

Identities = 216/236 (91%), Positives = 225/236 (94%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSY-LAWYQQK 59
ME PAQLLFLLLLWLPD TTGEIVLTQSP TLSPGERATLSCRASQS+SS LAWYQQK
Sbjct: 1 METPAQLLFLLLLWLPD TTGEIVLTQSPGTLSPGERATLSCRASQSISSSSLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPY-TF 118
PGQAP LLI+ AS+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQ+ ++P +F
Sbjct: 61 PGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGT+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
Sbjct: 121 GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g16741061 Similar to immunoglobulin kappa constant [Homo sapiens]
Length = 235

Score = 430 bits (1095), Expect = e-119

Identities = 214/235 (91%), Positives = 224/235 (95%), Gaps = 1/235 (0%)

Query: 1 MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQK 59
ME PAQLLFLLLLWLP TTGEIVLTQSPATLSLSPGERATLSCRASQ VSS YLAWYQQK
Sbjct: 1 METPAQLLFLLLLWLP GTTGEIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQK 60

Query: 60 PGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFG 119
PGQAPRLL++ +S+RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQY ++ TFG
Sbjct: 61 PGQAPRLLMFGSSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFG 120

Query: 120 QGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 179
GT+++IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
Sbjct: 121 PGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 180

Query: 180 QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Sbjct: 181 QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

>g23683336 immunoglobulin kappa light chain [Homo sapiens]
Length = 236

Score = 423 bits (1077), Expect = e-117

Identities = 213/236 (90%), Positives = 220/236 (92%), Gaps = 2/236 (0%)

Query: 1 MEAPAQLLFLLLLWLP--DTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ 58
ME PAQLLFLLLLWLP DTTGEIV+TQSPATLS+SPGERATLSCRASQSV S LAWYQQ
Sbjct: 1 METPAQLLFLLLLWLPVSDTTGEIVMTQSPATLSVSPGERATLSCRASQSVRSNLAWYQQ 60

Query: 59 KPGQAPRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTF 118
KPGQAPRLLIY AS RATGIP RFSGSGSGT+FTLTIS L+ ED A+YYCQQY TF
Sbjct: 61 KPGQAPRLLIYAASRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYNEWFRTF 120

Query: 119 GQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
GQGT++EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN

Sbjct: 121 GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

Query: 179 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 181 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

>g21669465 immunoglobulin kappa light chain VLJ region [Homo
sapiens]
Length = 265

Score = 415 bits (1055), Expect = e-115

Identities = 209/232 (90%), Positives = 213/232 (91%), Gaps = 1/232 (0%)

Query: 4 PAQLLFLLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA 63
P LLLL E LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA

Sbjct: 6 PTAAAGLLLLLAAQPAMAETTLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQA 65

Query: 64 PRLLIYDASN RATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTP-YTFGQGT 122
PRLLIYDASN RATGIP RFSGSGSGTDFTLTISRLEPED A+YYCQQY ++P YTFGQGT

Sbjct: 66 PRLLIYDASN RATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGT 125

Query: 123 RLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES 182
+LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES

Sbjct: 126 KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES 185

Query: 183 VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sbjct: 186 VTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

Database: genpept137

Posted date: Sep 11, 2003 11:22 AM

Number of letters in database: 474,463,515

Number of sequences in database: 1,534,369

Lambda	K	H
0.314	0.129	0.377

Gapped Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 225373096

Number of Sequences: 1534369

Number of extensions: 8964668

Number of successful extensions: 79945

Number of sequences better than 10.0: 32966

Number of HSP's better than 10.0 without gapping: 14318

Number of HSP's successfully gapped in prelim test: 18648

Number of HSP's that attempted gapping in prelim test: 44709

Number of HSP's gapped (non-prelim): 35882

length of query: 234

length of database: 474,463,515

effective HSP length: 60

effective length of query: 174

effective length of database: 382,401,375

effective search space: 66537839250

effective search space used: 66537839250

T: 11

A: 40

X1: 16 (7.2 bits)

X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 42 (22.0 bits)

Graphical Viewer...

Submit sequences to:

